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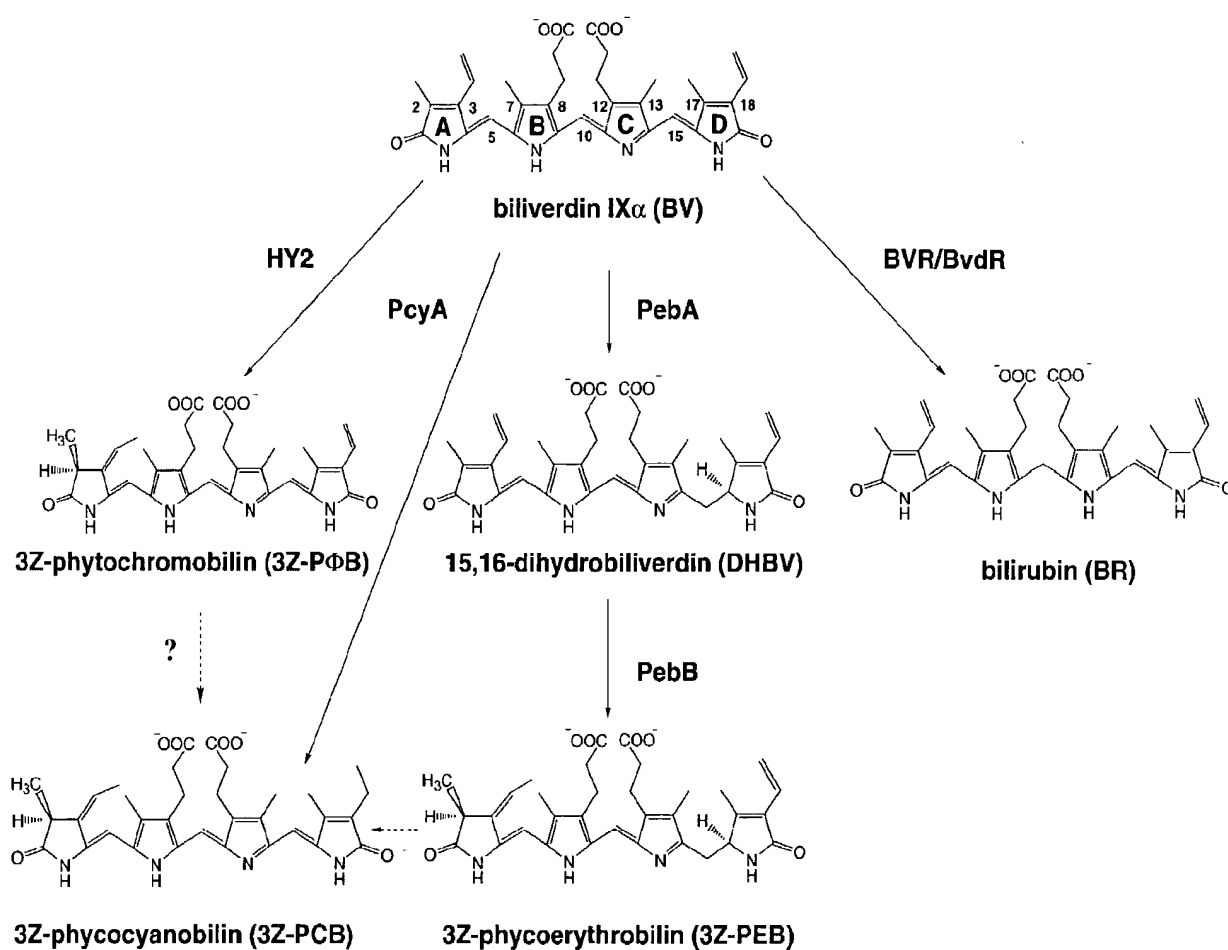


Fig. 1

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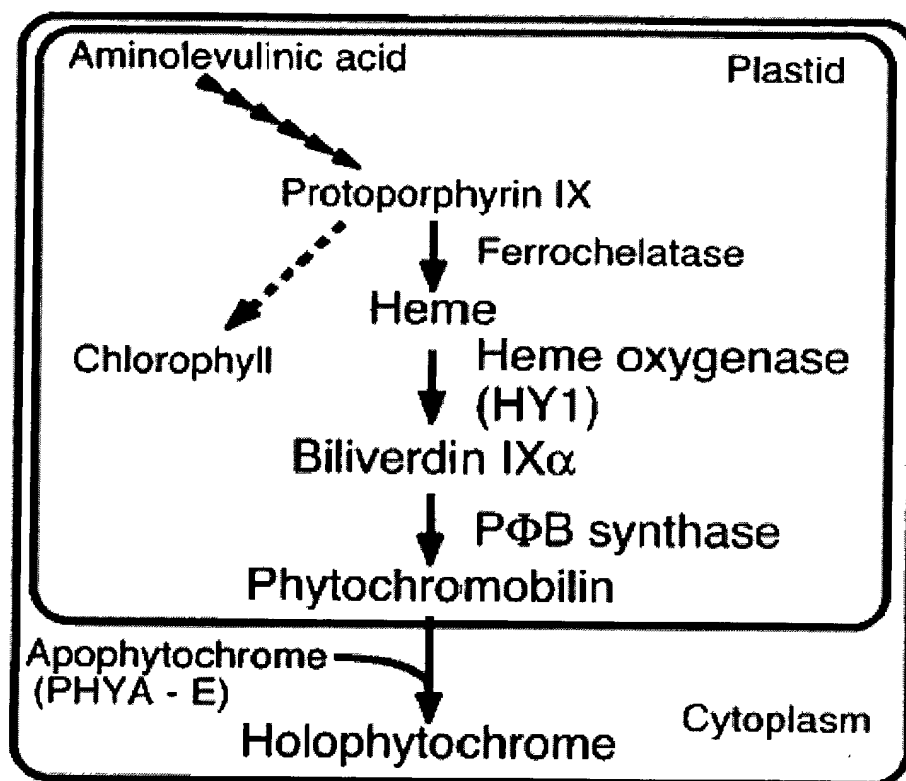


Fig. 2



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gaattccccacgtcaacgtgactgtgcattccacgtggcggatgtgggacctatagttgg 60
accatgactoggacggatgttgaaattcattgtcgttgccaattgcgtttgtctcactga 120
aactgtgaaaattttatctcttttatagataaAGAATCTTGCTTTTTTCAGTTTTTCAGTA 180
TGAAGAAGAATTGAAGAGAGTGTCCGAGGAAGGAGACCTTTGGTTTCAGTTTGTGAGTCT 240
TGTGTAAATGGCTTTATCAATGGAGTTTGGGTTTTCAATTGGGTCATGCTTCAAGGCACC 300
M A L S M E F G F S I G S C F K A P
AAACCCACCTGTTCTAATCTCTGCAAGCCCTAATAAGATCAATTTACGTTGAGAAGGAG 360
N P P V L I S A S P N K I N F T L R R R
AAAGAAAAGATTCTTACTTAGAGTCTCTGCTGTGTCTGATAAGGAATTCGCAGAGTCTGC 420
hy2-106 *****
K K R F L L R V S A V S Y K E F A E S A
TTTAGAAGAAACCAGGAAAAGGATCGTTCTTGAACCTTCACATCTCCAGgtatatgcaat 480
L E E T R K R I V L E P S H L Q
tacatttcgttagtgtagtgggaggattatatatttctcattgtttcttgctgtgaattttg 540
ggtaaattgatttgagttgtcattaggaaccaaaacaataactttactgttatagactgc 600
ttatataagtaaaagttcagatttttgtttttctaatacacgaaactgttttcagGAAAAGTA 660
E K Y
TAGTAGCATGACAGGACTAGATGGTAAGACCGAACTTCAAATGCTTGCTTTTAAATCTTC 720
S S M T G L D G K T E L Q M L A F K S S
AAAGATTAGACTCTTGAGGAGTATGGCAATAGAGAATGAGACAATGCAGgtttaacttca 780
K I R L L R S M A I E N E T M Q
gcagtacaaactgattgcttttagtcccatttccttactttcaattgattgattgtttgta 840
hy2-105 *****
tcttcgcttagGTCTTTGACTTTGCGGGTTTCATGGAGCCTGAGTATGATACTCCCATAT 900
hy2-1,hy2-104 T
V F D F A G F M E P E Y D T P I F
TCTGTGCTAACTTTTTTCACATCTACCAACGTTAACATAGTTGTATTgtaagttatcttct 960
C A N F F T S T N V N I V V L
agttatgctggagttatcaggtctgtattgtccaaactgatgttcaatattttactgtat 1020

Fig. 3B



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gttcttcttttagGGACCTTAATCCTTTGCATCAGTTGACTGACCAGACGGATTACCAAGA 1080
D L N P L H Q L T D Q T D Y Q D
CAAGTATTATAACAAGATAATGTCCATATATCACAAATATGCTGAGgtgaccacaangaat 1140
K Y Y N K I M S I Y H K Y A E
acaccaaattactcaattgcaagtaaaccotaatgctgaggtgtaaatgactgatcttgag 1200
atttatttgcagACTTTCCCATGGGGAGGGAAATTGACTGGTGAATCCATAAAGTTTTC 1260
hy2-101 A
T F P W G G K L T G E S I K F F
TCGCCTTTGGTGATGTGGACTAGGTTTTCGTCTAGCAAAGAAAAACATAAGGCTTTGTTTC 1320
S P L V M W T R F S S S K E K H K A L F
TCTGCGTTTCTAGAGTACTATCAGgtatatactcagcgggccaaaagctaagggtttttattg 1380
S A F L E Y Y Q
gaaactttgactgagaatctatcatcttcttcttctacagGCATGGCTTGAGATGACAATCC 1440
hy2-107 a
A W L E M T I Q
AAGTGAGGGAGGAGATGGAACCATCTCATGTGAGAGCCAATTGTGAAGCACAACACAAGT 1500
V R E E M E P S H V R A N C E A Q H K Y
ACCTGACATGGCGAGCACAAAAGgtgatttcatttcttttgtgtaatttgcaggtttga 1560
hy2-103 A
L T W R A Q K
acagacactgtatctgtattgttacaantggatattgatttggtggttgagGATCCTGGA 1620
hy2-102 a
D P G
CATGGTCTTCTTAAAAGATTAGTAGGTGAAGCAAAGGCAAAGgtataaaaagatttgatcc 1680
H G L L K R L V G E A K A K
cattagtggtccccattattaattagcttgtgaagatggttgaaaatgatttgaacaaaatc 1740
agGAGCTGCTAAGGGATTTCCTGTTCAATGGGGTGGATGAGTTAGGCACAAAAACATTCA 1800
E L L R D F L F N G V D E L G T K T F I
TTGATTACTTTCCAGAGTACCAAACAGAAGATGGAAGTGTAAAGCGATAAACGAAGTATCA 1860
D Y F P E Y Q T E D G T V S D K R S I I
TTGGGAAGTCATATGAAACTCGTCCATGGGATTTAACAGGACAATTTATCGGCTAACAAAT 1920
G K S Y E T R P W D L T G Q F I G ==
GATATATGTGAACAAGTCAGATTTTCAGAGTCATCAACACAAGAGGACGTGAACCTTAGGGA 1980
AGTAGGAATAAGAAAGAGCAGCATGAGGAGTCTCTCAGGTCTATCTGCATTTCAAGATGA 2040
TTGTTTGAGTTACCATGCATTGTAGTTTTACAAGTGTAGCTCTCAGCCCTTCATCAAAAT 2100
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Fig. 3B cont'd.



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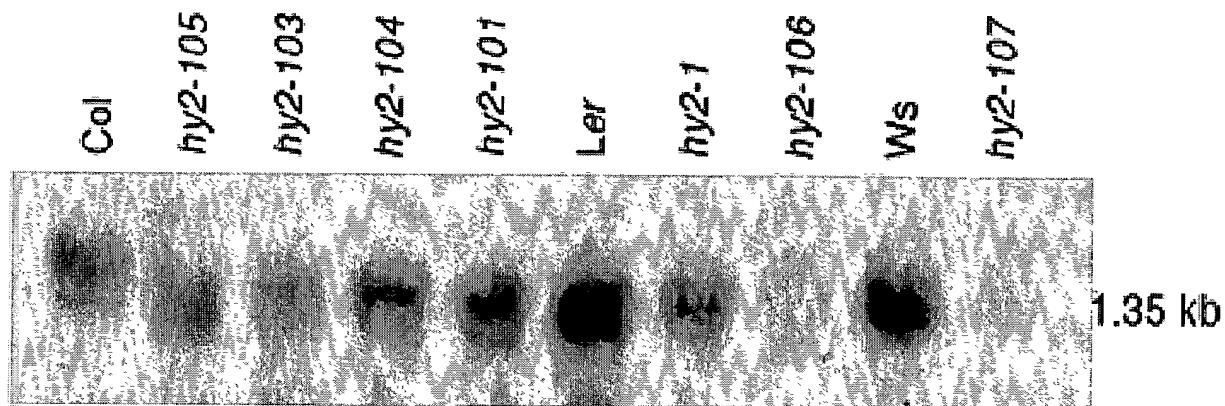


Fig. 4A

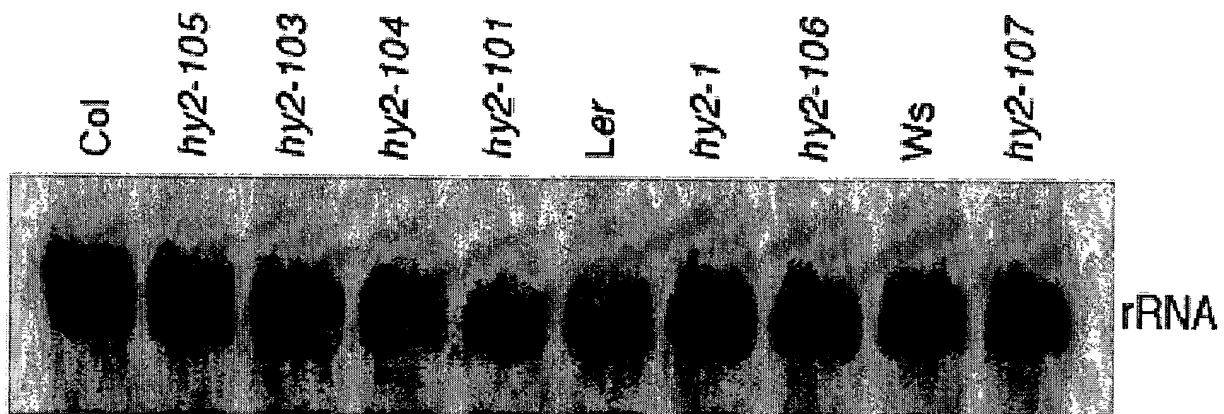


Fig. 4B



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* 20 *

HY2_ARATH : MALSMEFGFSIGSCFKAPNPPVLI SASPNKINFTLRRRKK
YCP2_SYNPY : -----
YHP2_PROMA : -----
YHP3_PROMA : -----MI I KR DNS
YCP3_SYNPY : -----MTNQRFKS
SLR0116 : -----MAVTDLSLTN

* 60 *

RFLLR SAVSYKEFAESALEETRKRI VLEESHLEQEKYSSMTGLDGK : 86
-----FDSFLNELHSDITKR-----GGSELEPEGLEECRSSKSS : 36
-----LNKLMLQDLHNNLKRI-I SHGCKPIEVENGMSERFSHKQD : 40
LSKID ERDWIWT PFFNDLV DKL-SVFEIEPYPVSHDFLSKESITGSR : 54
TDPVNIEGWSWQPFLEDAIKRL-EGLNVEPYPVPDRFLQREDQTGSK : 54
SSLMPTLNPMIQQLALALIAASW-QSLPLKPYQLPEDLGYVEGRLEGE : 56
P 6

* 100 *

HY2_ARATH : -----TELQMLAEKSSKRIQLLRSMADEN-ETMQVDFDFAGE
YCP2_SYNPY : -----SVIQSWLWDVPGFRRWRVTRDAGDSQVENS VAY
YHP2_PROMA : -----TVIKSWLWDVPGFRRWRVTRDAGDKQVLS VAY
YHP3_PROMA : RNPVHVTTLTWAAKFEKIKQVRLACIKGSESLSVFNLIH
YCP3_SYNPY : SKSIPVTTATWACKTEKFRQVLAACYSAGSAASVLFNIN
SLR0116 : -K-----LVLENRCYQTPQFRKMHLLELAKVKGQDLHCVMF
4 f g 6

* 140 *

MEPEYDTPIFCANFFFTSTNVN-----VVMIDLNEHLHQLTDQTDYQDKYAN : 165
PDYNDRPLMGVDLWFGARQKLAVVDFQPLVQ---DKDYLDRYES : 115
PAYTNDKPIILGIDIFWFG LKRKLAVVDFQPLVQ---EERYFCRYK : 119
PLNDV DLEFFGADFWTL PNG--HLLADLQPAKL--DNIHTENVVP : 137
PKSTYGLFFFGGLVTFPAG--HLLADLQPAKT--DEVHTTHVD : 137
PEPLMGLFLFGCDIVAGPGG-VSAATADLSBTQS---DRQLPAAYQK : 135
P Y P g l 1 D P

Fig. 5



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```
180          *          200          *
HY2_ARATH   : KIM----SYHKVAETTPWGCKLTGESIKESPLVMTR-
YCP2_SYNPY  : GLK----EYNQRIPDLNGEETMRSTDPNQYESSWLLTCR-
YHP2_PROMA  : DLQ----ILKNRIVDFNSQKTMKIYDSNKIESPWVLLYN-
YHP3_PROMA  : RLI----PLHDHMQSLLPSGGEIPKEAEFYESPGLSRL
YCP3_SYNPY  : RLI----PLFERWRDQLPYGGPIPEEAQFEESPGLMTRL
SLR0116     : SLAELGQPEFEQQRELPPWG-----EIESEYCLAIR-
              6                      FS      6      r
```

```
220          *          240          *          260
---FSSSKEKHKAIFSAFLEYVYQANLEMTIQVREEMEPSHVRANCA : 244
---GGAEQADLSMPKATSAIKAYWDIHDNAKSIPSTIPPEEVKNL : 193
---GSFDDLQCSIAKILDEIHAHWQNDNNNSREYIKIIPSKVEGL : 197
PLSKESDNIISEIRPAFGEYISLYIEILHIAKPLKKER-ALKILEG : 219
PLGEEGDELIQSIRPAFENDYLDLLELAASAERVTDER-SEVLLLG : 219
----PSNVTEERFVQRVVDLQIHCHQSIVAEPLSEAO-TLEHRLG : 208
              51
```

```
          *          280          *          300
HY2_ARATH   : QHKYLTTRAQKDPGHGLKKRLVCEAKAKELLRDFLENGVD
YCP2_SYNPY  : QDKYDIYSAERDPAHGLFTSHFGKDWSNRELHEFLGPASS
YHP2_PROMA  : HINIDIYSAERDPAHGLFKSYFCQTADQGVREFLEPHSH
YHP3_PROMA  : QKATINRSTKDFARAMLCRFYCKEWTEDEYHKVLENI--
YCP3_SYNPY  : QRKYTDYRAEKDPAARGMLTREHCSSEYTEAMIHTVLEDDL--
SLR0116     : QIHYCQQQOKNNDKTRRYLEKAFGEAATAERMMSQVLEDDVIQ
              q      Y          Dp      6      G      W      6      LF
```

```
          *          320          *          340
ELGTKTFIDYFPEYQTEDGTVSDKRSIIGKSYETRPWDLTGQFIG : 329
SHK----- : 236
LTAD----- : 241
----- : 257
----- : 257
----- : 248
```

Fig. 5 cont'd.



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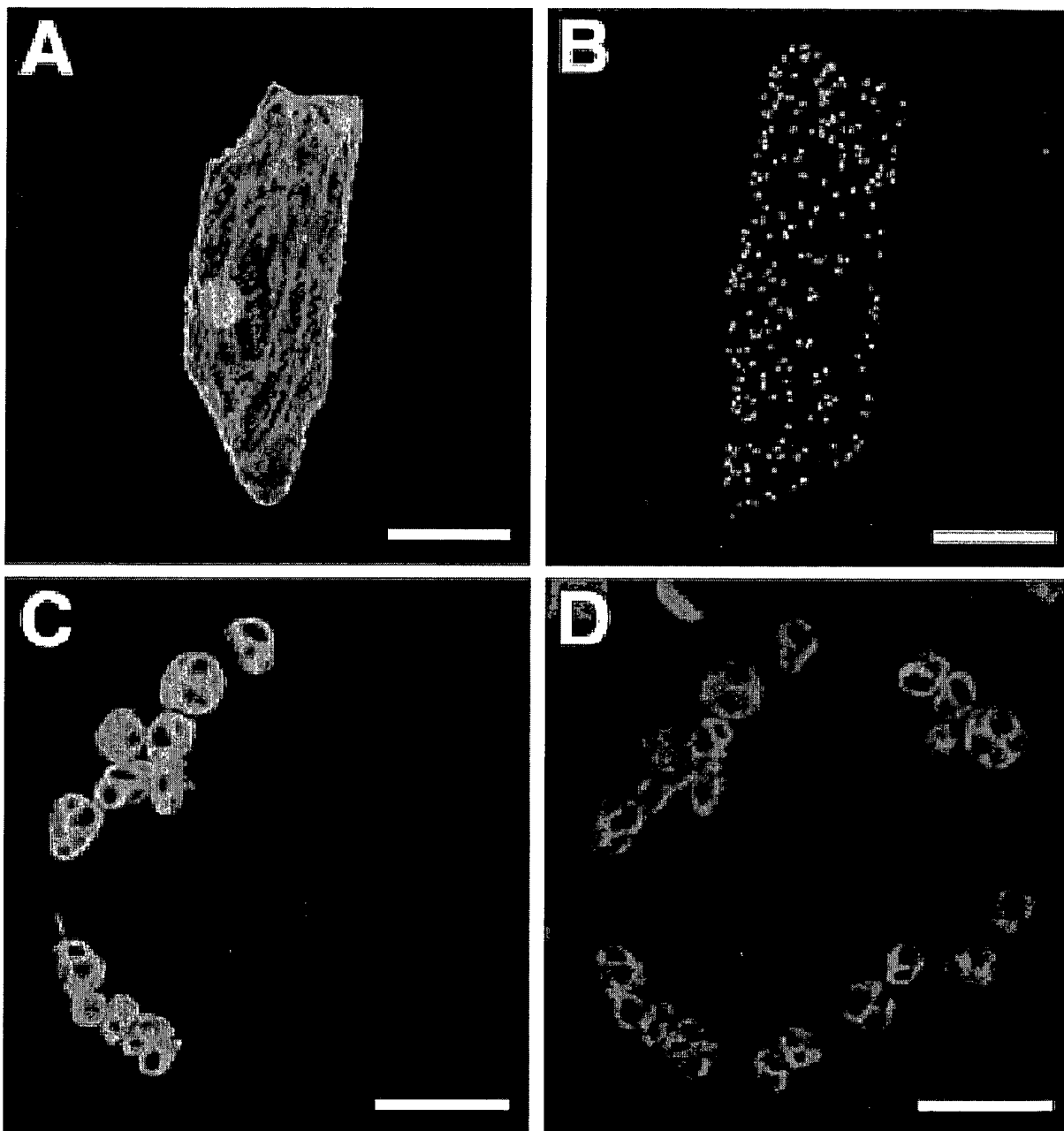
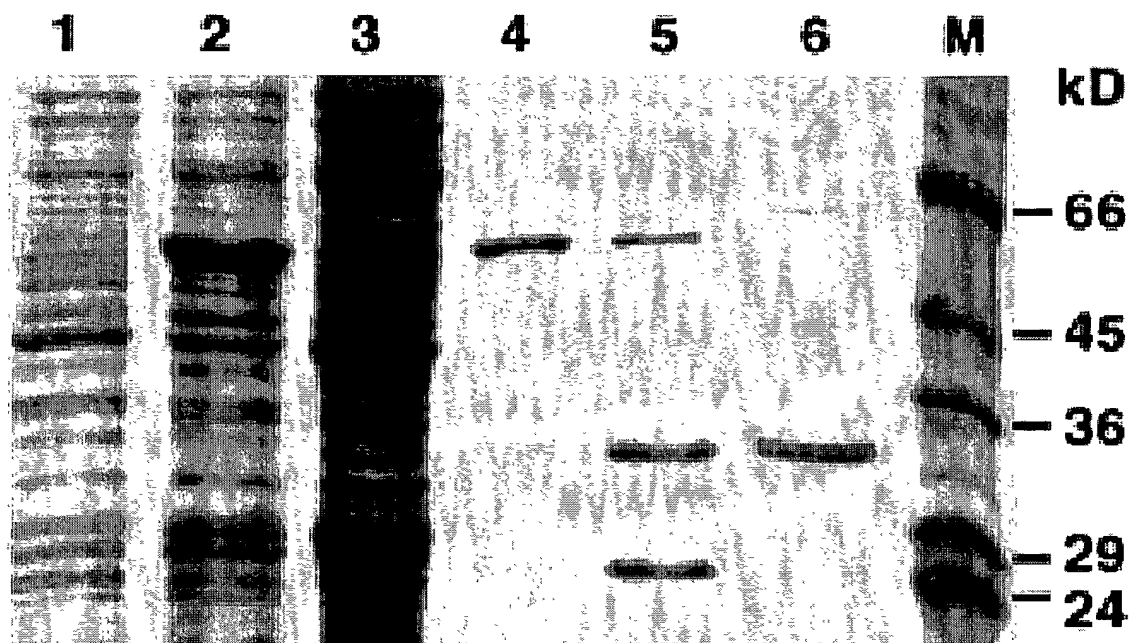


Fig. 6



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*Fig. 7*



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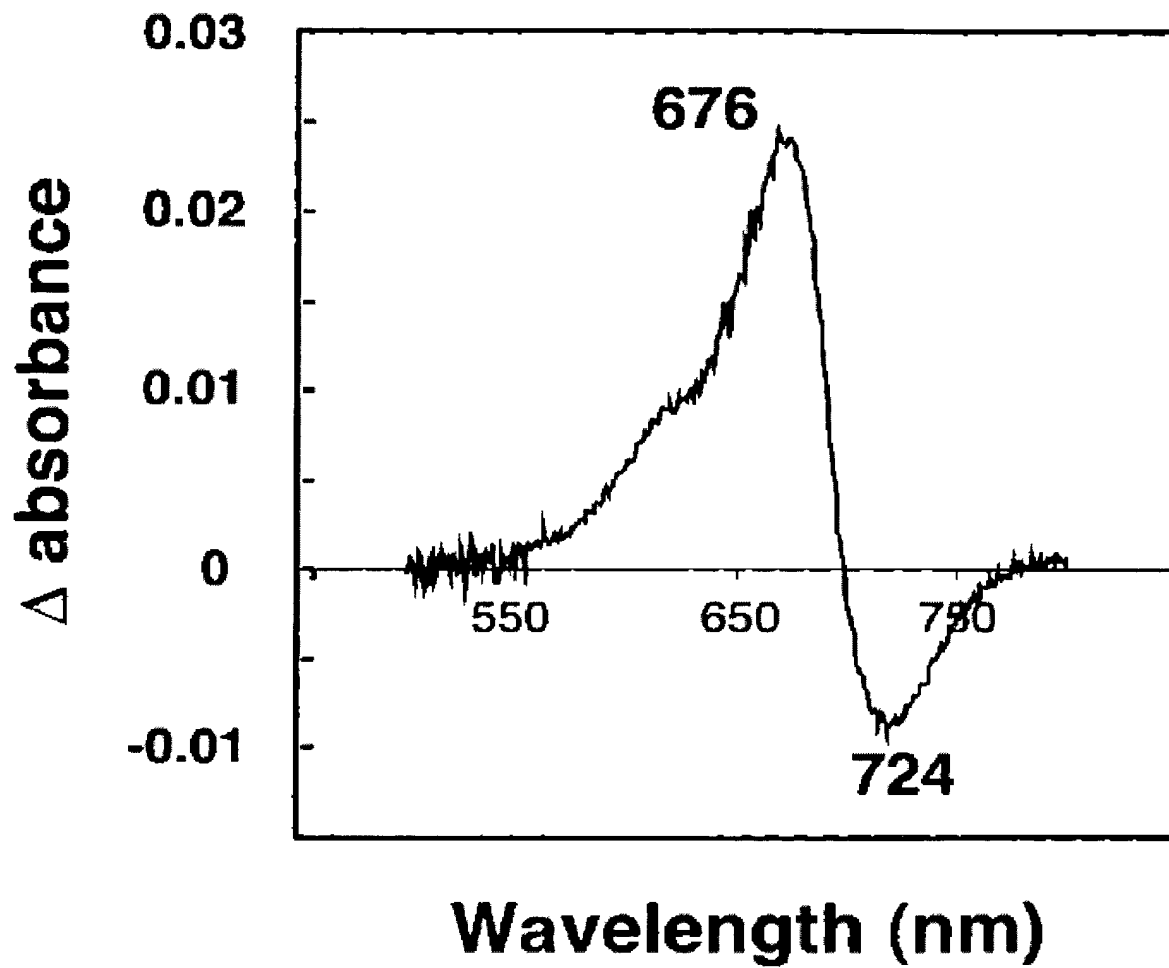


Fig. 8



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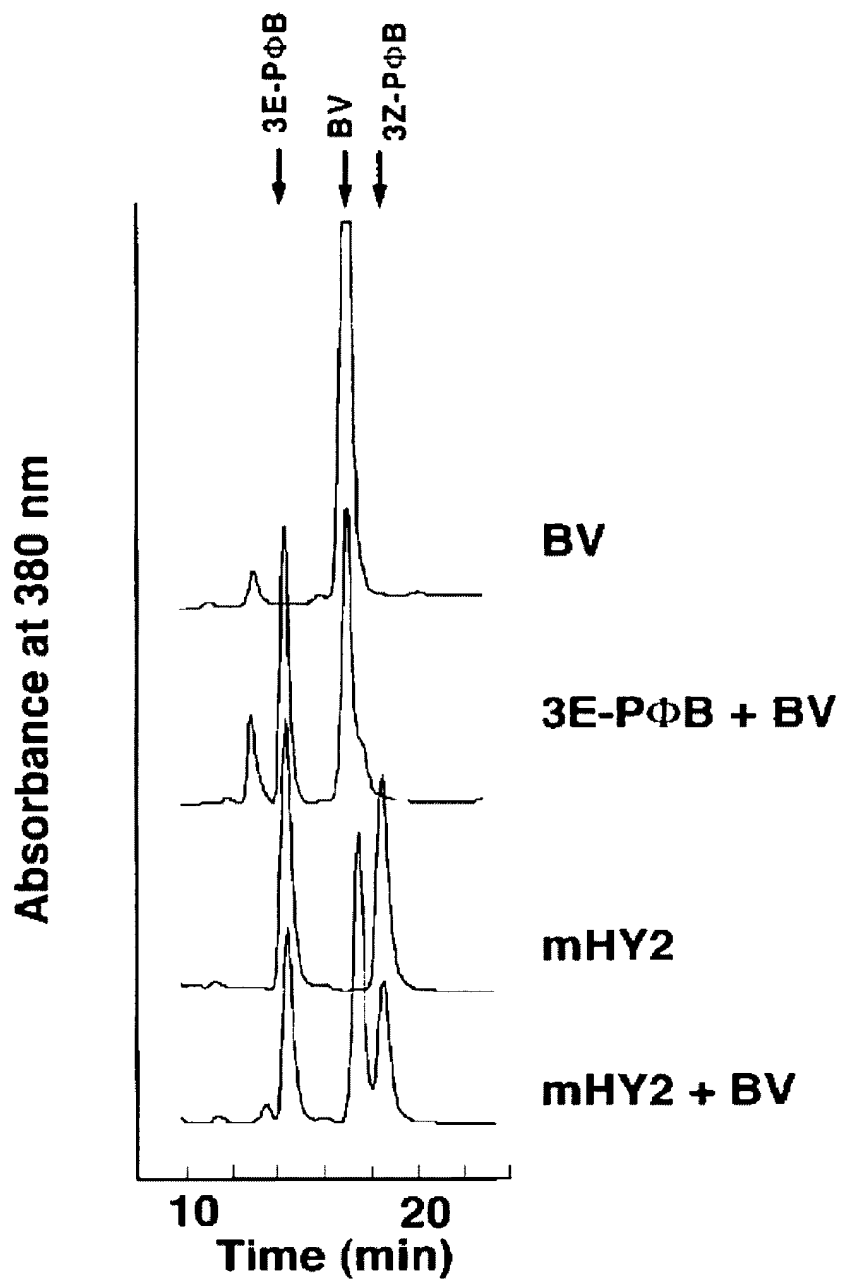
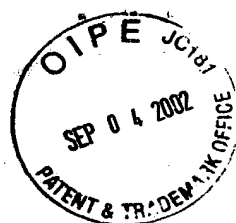


Fig. 9



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```

*                20                *                40
Pcya_ANASP : -----
Pcya_NOSPU : -----
Pcya_SYNY3 : -----
Pcya_SYNB1 : -----
Pcya_PROMA : -----
Peba_SYNPY : -----
Peba_SYNB1 : -----
Peba_PROMA : -----
Peba_PROMA : -----
Peba_NOSPU : -----
PebB_SYNPY : -----
PebB_SYNB1 : -----
PebB_PROMA : -----
PebB_PROMA : -----
PebB_NOSPU : -----
HY2_ARATH : -----
RCCR_ARATH : MAMIFCNTLYSSSSPSYLSPLTSKPSRFSKNLRPRAQFQS
RCCR_HORVU : -----

```

```

*                60                *                80                *
-----MSLTSIPSLREQQHPPIRQLADCHIEVWHQHLDLSPYHHPAEL : 43
-----MSFTMPSLREQQHPPIRQLADCHIEAANHQHLDLSPYHHPDEL : 43
--MAVTDLSLTNSSLMPTLNPMIQQALALATAASNQS-LPLKPYQLPEDL : 46
-----MQSPPESSSSTVAPMILPSLAETURGAWIGLPELKPLDADSDF : 42
-----LNLLSRSLTKTKLIDPILTLTLLQNTKVKVQRSKLNDLNCIEVDPKL : 44
-----MFDSPLNEHSDITK-RGGSPLEFLPEGL : 27
-----MFDPFLEELGTGTOA-RGGISVEVPAGL : 27
-----MNKLLQLDLHNNKRRFIS-HGGKRIEVENGM : 31
-----MFESLKNFMKTNIE--DLDGKELEISK : 25
INETCMIAITYFHARVKNKSCSYKPFLEFLKELFQRFDLQSRVPIPEGL : 64
----MTNQRFKSTDPVNIEGWSWQPFLDATKRLLEG-LNVERYPVPDFR : 44
--MSIDLRASSLDPVQIPGWEWQPFLDEASAAKLP-FNPSYPPIAETF : 45
----MIIKRDMSLSKIDLRDWTPTPFNDVVDKLSV-FETIEYPVSHDF : 44
-----MLIQNTIFYSQEWRWAKFIKFIISQLDN-YHCVENKIASDF : 40
-----MNSERSDVTYQPFLDYAIAYMRSRLDLEYPPIPTGF : 37
KINFTLRRRKERFLLRVSAVSYPEFAESAEETRKR-IVLEPSHLQEKY : 77
HDDHLRRKFMEFPYVSPTRKQIMVDLMSTVENRLQS--QLLPCNLPDPV : 90
-----

```

Fig. 10



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          100          *          120          *
PcyA_ANASP : GYVEGRLEGEK-----LTLENRCYQTPQFKKMHLELAKV
PcyA_NOSPU : GYVEGRLEGEK-----LTLENRCYQTPQFKKMHLELANI
PcyA_SYNY3 : GYVEGRLEGEK-----LVLENRCYQTPQFKKMHLELAKV
PcyA_SYN81 : SSIEGOLEGDD-----LLIRNELLCRCGVKKIHLELARL
PcyA_PROME : SNIISNEEGKE-----LYTENEFYKAKCFKKLHIEVAEFS
Peba_SYNPY : EECRSSKSS-----SVIQSWLWDVPCFRRNRVTRLDA
Peba_SYN81 : EHNQSQKGS-----STIQSWLWQVPCFRRNRVTRLDA
Peba_PROMA : SERFSHKQD-----TVIKSWLWDVPCFRRNRVTRMDA
Peba_PROME : EFKEHHNKD-----SKYILKNWIFESQQYKKWRITKLDG
Peba_NOSPU : EFKVSDRGR-----NPATIRSWCYQSOELKKIRYTYIDA
Pebb_SYNPY : LQREDQTGSKSK-SIPVTTATWACKTEKFQVRAACVSA
Pebb_SYNR1 : LQKEGSTGSKAK-PVPVTTATWACSTDKLQVRCACVEA
Pebb_PROMA : LSKESITGSRN-PVHVTTLTWAAKFEKIQVRLACEK
Pebb_PROME : SYKESSYGSKKS-KKNINLFTWGATHQKRINFARAVCINS
Pebb_NOSPU : ESNSAVVGKGN-QEEVVTTSYAFQTARLQVRAAHVQC
HY2_ARATH : SSMTGLDG-----KTELQMLAEKSSKIELLSMAIEN-
RCCR_ARATH : RNFNNPNGSAEASLHIRSGDKSSPIDFVIGSWIHCKIPTC
RCCR_HORVU : -----MDFMLQSSSLHCKVPN

```

9

```

          140          *          160          *          180
NMEDILHCVMEFPRPEYDLPMFECDLVGGGR-GQISAAADLSSVHL---BRTL : 126
NMEDILHCVMEFPRPQNNLPMFECDLVGGGR-GQISAAADLSPIQL---BRTL : 126
KGLDILHCVMEFPEPLYGLPFECCDLVAGP-GGVSAADLSPTQS---DRQL : 129
RGLOILHCVMEFPDPRFDLPFECADLVAGP-AGVSAADLSSPV---SGTL : 123
KSLKILHCVMEFPDPKYDIPFEGMDLVKVN-ELVSAADLSSSK---NQNL : 127
DSLQVNSVAMPDYNMDHPLMGVDLLWFGARQKLAVLDFQPLVQ---DKDY : 109
DSLQVNSVAMPDFDLDPHPLMGVDLLWFGARQKLAVLDFQPLVQ---DKDY : 109
DKLQVNSVAMPAYTNDKPILEIDLLWFGLKRKLAVLDFQPLVQ---BRY : 113
DKLQVNTVARENFKSEFPILCADLLWFGTSQKLLAFDYFQPLIQ---BKKY : 109
ESAQIFNSVWYPSHNYDLPLLGIDLLSFG-KVKNLIVLDFQPLFQ---DEDY : 147
SAASVLENFVINPKSTYGLPFEGGDLVTFP--AGHLLALDLQPAIK--TDEVH : 131
MAASVLENFVINPSCREDEPFEGADLVTLP--NGHLLALDLQPVOK--ADPDH : 132
ESSEVFNLLIHPLNDYDLPEFGADLVTLP--NGHLLALDLQPAIK--LDNIH : 131
FNYSVLENFLLIPKTSYNIPFLGVDLVSLP--TSHLLVLDFQPSLK--VENQF : 127
NSLQVENFVIEFHLNYDLPEFGADLVTLP--GGHLLALDLQPLFR--DESAY : 124
ETMQVFDFAGMEPEYDTPFECANFETST--MVNIVVLDLNPLHQLTDQTDY : 159
VSLNITSISGRLNSSTKAPNEVELIQSS-SKSLVLILLDLPHRKDLVLNPDY : 181
-ADLITSLFINLNASTDAPHEIMEFIQGS-PTSMVLILLDLPRKDLALHPEY : 66

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4

p

P

g

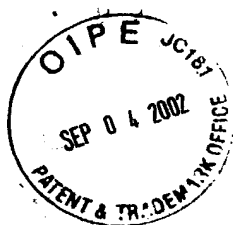
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4

D

P

Fig. 10 cont'd.



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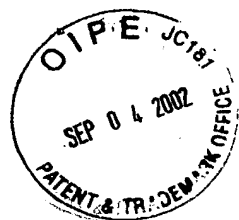
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*               200               *               220
PcyA_ANASP : PESYNSA L T S I N T - - - - L N F S Q P R E L P I W G N I - - - - F S D F
PcyA_NOSPU : PESYTTA L A Q L P V - - - - L N F S Q P R E L P I W G N I - - - - F S D F
PcyA_SYNY3 : P A A Y Q K S L A E L G Q - - - - P E F E Q Q R E L P P W G E I - - - - F S E Y
PcyA_SYNB1 : P S G I E T A L A G T P S - - - - P A F R Q V R D L P G W G T I - - - - F S P W
PcyA_PROME : - - K Y D H L L S H L D K - - - - S V F K S K R E I P I W G N I - - - - F S K N
PebA_SYNPY : L D R Y F S G L K E L N Q R F P D L N G E E T M R S F D P N Q - - - - F S S W
PebA_SYNB1 : L D R H F D G L K D L N A R F P D L N G E E T M R S F D P N Q - - - - F S S W
PebA_PROMA : F C R Y Y K D L Q I L K N R F V D F N S Q K T M K I Y D S N K - - - - F S P W
PebA_PROME : L Q K Y C S S L D F L K N O Y S V F D N H K M K N I Y D S K K - - - - F S P W
PebA_NOSPU : Q N K Y I A P L K Y L H N K Y P D L A Q N L E M K F Y A N Q - - - - F S K Y
PebB_SYNPY : T T H V W D R L I P I F E R W R D Q L P Y G G P I P E A Q P - - - - F S P G
PebB_SYNB1 : T Q F V W E R L M P I F E R W Q A E L P D G G T I F E A Q P - - - - F S P A
PebB_PROMA : T E N V W P R L I P I H D H W Q S L L P S G G E I P K A E P - - - - F S P G
PebB_PROME : N S E L L E Q I I K L K S C H S S L P V A E K M S E V A K - - - - F S P G
PebB_NOSPU : Q A K Y T E P I L P I F H A H Q Q H L S W G G D F P E A Q P - - - - F S P A
HY2_ARATH : Q D K Y Y N K I M S L Y H K Y A E T F P W G G K L T G S I K - - - - F S P L
RCCR_ARATH : L K E Y Y Q D T A L D S H R Q S L L K L P E V N D Y V S P S L F V R S A F S P T
RCCR_HORVU : I E K Y Y E D T E V D K Q R K I I E Q L P Q A R P Y L S P S L F V R S A F S P T
4
FS
```

```

*               240               *               260               *
C D V R P - - - - - S S P E E E A M F I G R V R E P I Q V H C Q G A I A A - - S P V S A E Q K : 199
C D V R P - - - - - G S P E E E A M F L S R V R E P I D I H C M Q A I A S - - H P V S V E Q V : 199
C D F I R P - - - - - S N V T E E E R F V Q R V V D E L Q I H C H Q S I V A - - E P L S E A Q T : 202
M C D I R P - - - - - D G A E E E V L F R S R V E E V I P I L R T A V I Q T A C E P A T A A S T : 198
M F P A S L - - - - - K N E S E K N A F C K I V D N Y L S V L I Q L S Q S T - - S P D S D Y E I : 198
I L D F C R G - - - - - G A E Q A D L S L P K A F S A F L K A Y W D L H D N A - - K S I P S T I P : 186
I L D F C R G - - - - - G S E E A D R S L P K A F S A F L K A Y W G L H D E A - - S K E P S S I S : 186
W L R Y N G - - - - - S F D D L Q C S L A K I L D E F L H A Y W Q V D N N N - - S R E Y I K I I : 190
W M I C R G - - - - - N K I N L D R D L N N I F C S E V S N Y L T I N K I H - - - O N N O F L D : 185
L D F A K T - - - - - D A E T V S T R V F E A F O D Y L N L Y W Q M L A D A - - Q A E H D P E D : 224
F L W T R L P L G E - - - - E G D E L I Q S I V R P A F N E Y I D E Y L E L A A S A - - E R V T D E R S : 213
F L W T R I P L G E - - - - E G D E L I E R V I R P A F I D Y L Q I Y L N L V A E A - - E P V S D D R A : 214
F L W S R L P L S K - - - - E S D N I I S E I L R P A F G E Y L S L Y I E L L H I A - - K P L K K E R A : 213
I L W S R I A K H Q - - - - D S D N L I E N Q L Y D S F K E Y L N L Y L K T L F E S - - E E V G H G I Q : 209
F L W T R P - - - - - Q E T A V V E T Q V F A A F K D Y L K A Y L D F V E Q A - - E A V T D S Q N : 202
V M W T R F - - - - - S S S K E K H K A L P S A F L E Y Y Q A W L E M T I Q V - - R E E M E P S H : 237
A S M L K I D A E E - - E D K L E S I L R D H V S P A A K E V I E V L E R C V K E E E K I V V C E E : 271
A W S F T I D C G R G C E G T L E E I V H G H L A S V V K G I L Q I W L D T C A S D - - - A S E M E E G : 155
4
```

Fig. 10 cont'd.



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280          *          300          *
PcyA_ANASP : OOIFA-GOHNYCTSKOOONDKTRRVLEKAFGVDDAENVMYMTT
PcyA_NOSPU : TQNEFA-GOHNYCTKQQQONDKTRRVLEKAFGPPVVAENVMYMTT
PcyA_SYNY3 : LEHRQ-GOTHYCTQQQQQKNDKTRRVLEKAFGEAAVAERYNSQ
PcyA_SYNB1 : IRRYE-GOLSYCLQQKRNDKTRRVLEKAFEDASVADRZYIEE
PcyA_PROME : IEERINYCKNYCVQOMKNKTSLSVLLKYEFDKVVVDEYIEK
PebA_SYNPY : PEEVKNLQDKYDIYSAERDPAHGIFTSHFGKDDSNRELHE
PebA_SYNB1 : PGDVERLQNAVQVYSAERDPAHGIFTSHFGKEDSDRELHE
PebA_PROMA : PSKVEQLHINYDIYSAERDPAHGIFKSYFGQTWADQEVRE
PebA_PROME : LEQIKNNQIDYOKYSAEKDPADKLFKTFEGGTWTENFINN
PebA_NOSPU : IQRTVKAQKDYQOYSADRDPASGIFSSSYFGHEVAERELHE
PebB_SYNPY : EVLLQ-GORKYTDYRAEKDPARGMLTRFHGSEMTTEALHT
PebB_SYNB1 : ELLPS-GOKRYTAYRAEKDPARGMLTRFYGSEMTESYIHG
PebB_PROMA : LKILE-GOKAYINRSTKDPARAMLCRFYGKEMTEDYIHK
PebB_PROME : QELIN-GANDYLNRRDNDPARPMLS SLFGKDETESLINK
PebB_NOSPU : LVAIKQAQLRYLRYRAEKDPARGMFKRFYGAEMTEYIHG
HY2_ARATH : VRANCEACHKYLTWRAQKDPGHGELKRLVGEAKAKELLRD
RCCR_ARATH : ERMELERRDKSPRKSIEVDLDLQFPRMEGGEVSRVVAHA
RCCR_HORVU : EREIMVKRDRTVRSKSIEVOLTANLPRMEGCPDVSGRITAE
          q    Y          1    4    3G    4
```

```
320          *          340          *          360
VLFDLPE-----: 245
VLFDLPT-----: 245
VLFDV1Q-----: 248
VLFDPLPFG-----: 247
VLFDL-----: 243
FLFPASSSHK-----: 236
FLFPSQPA-----: 235
FLFPHSHLTAD-----: 241
FLFPLNHNPLK-----: 236
FLFEDAVPLAVSASKR-----: 280
VLFDL-----: 257
VLFDLEDA-----: 262
VLFDNI-----: 257
VLFDTNKVL-----: 257
FLFDLERKLTVVK-----: 255
FLFNGVDELGTRTFIDYFPEYQTEGTVSDKRSITIGKSYETRPWDLTGQFIG : 329
TRKAFGVL-----: 319
TRKAFGVQEG-----: 205
LF
```

Fig. 10 cont'd.



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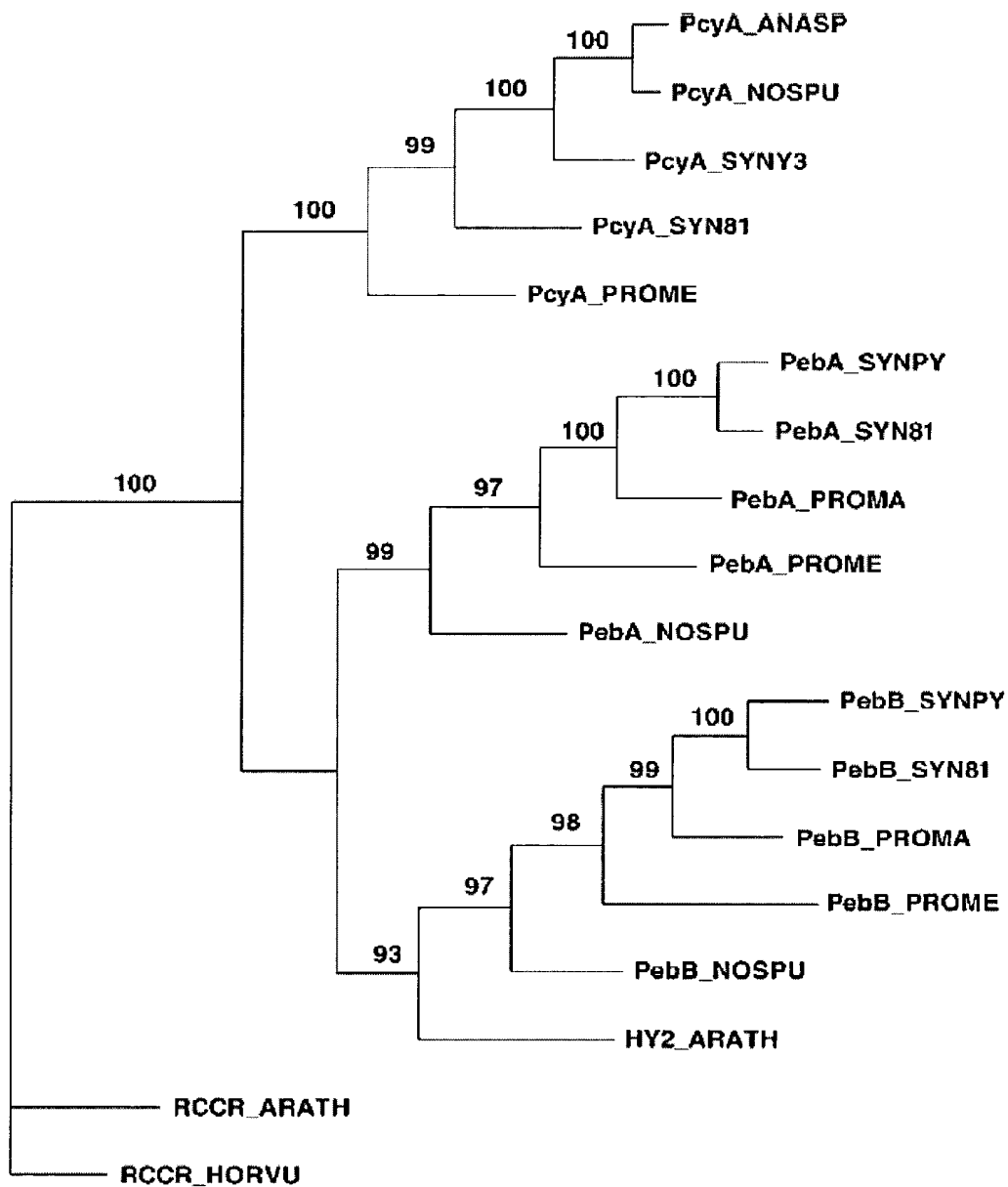


Fig. 11



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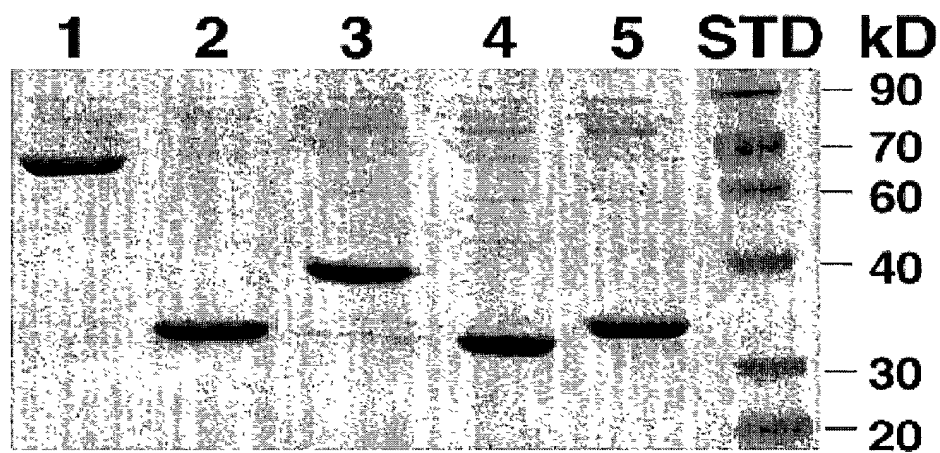


Fig. 12

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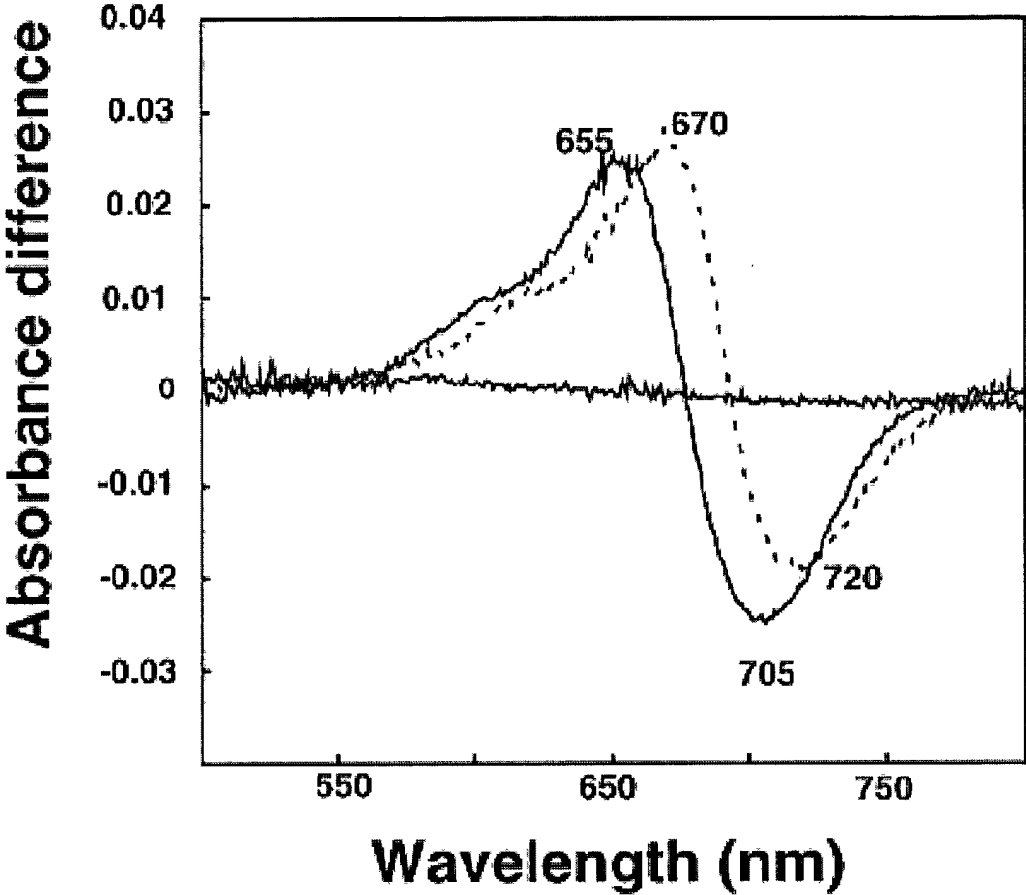


Fig. 13A



09870406 .090402

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Normalized fluorescence

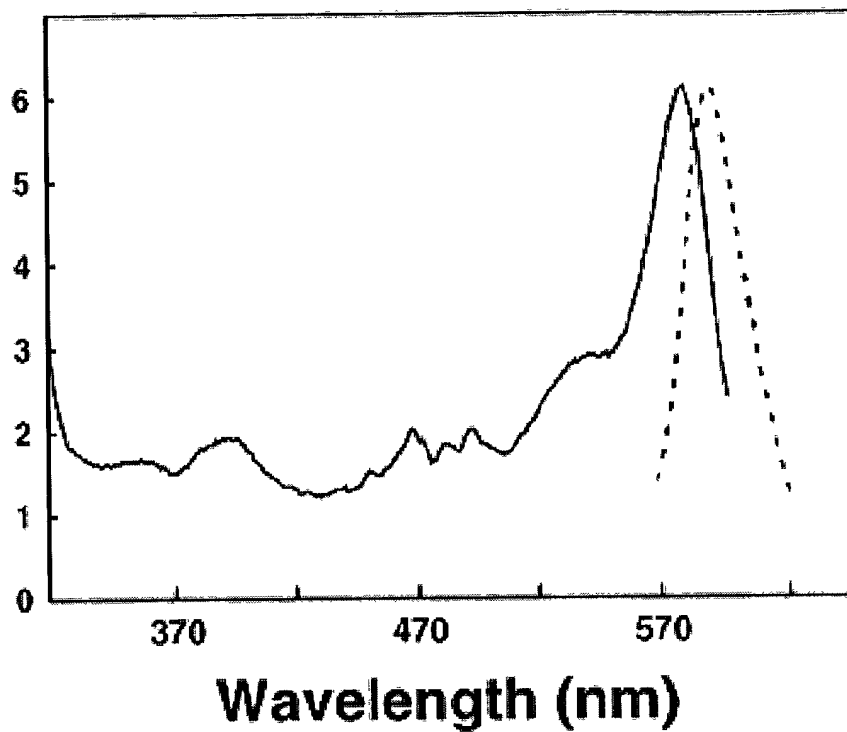


Fig. 13B



09870406 090402

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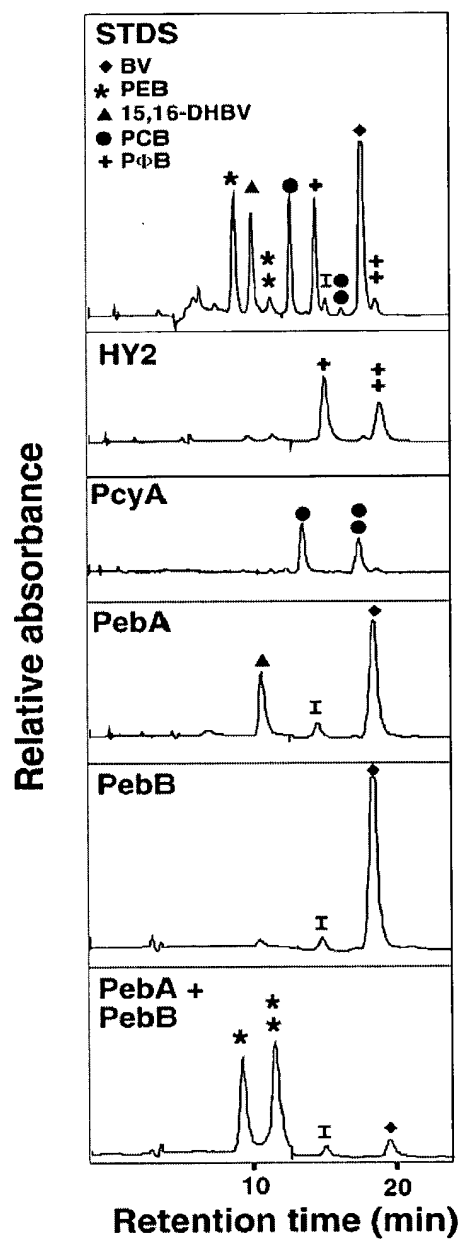


Fig. 14



099370406 .0190402

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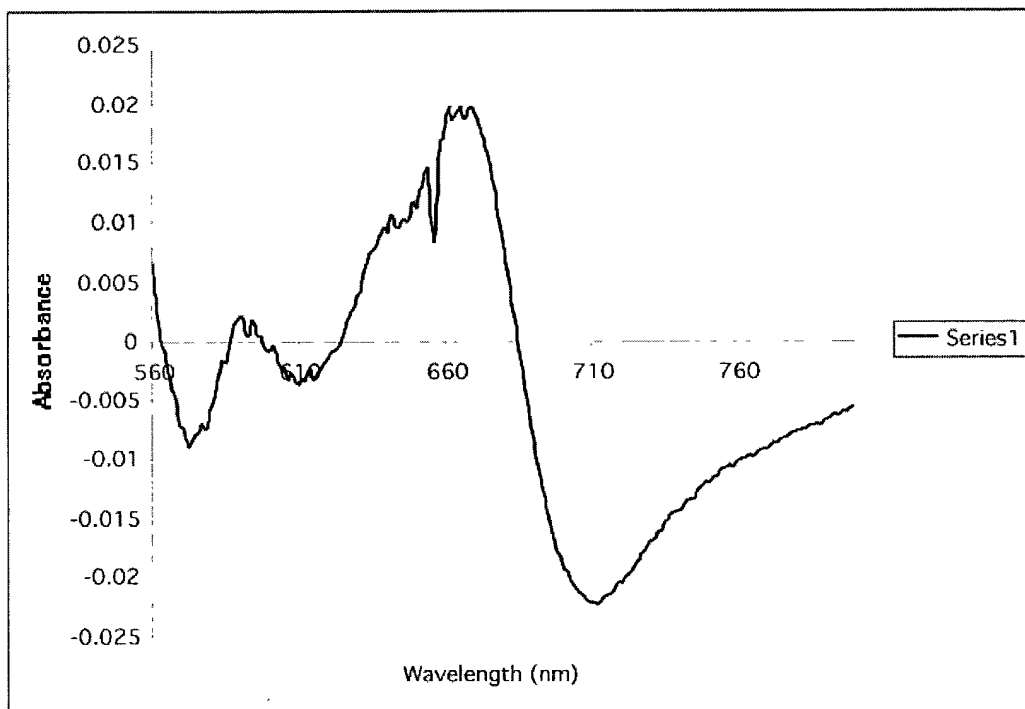


Fig. 15

Fig. 16